

G. Bugaisky

4/10

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/439,740

DATE: 05/05/2001
TIME: 00:04:53

INPUT SET: S36631.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: FUNK, Walter D.
6 MacGILLIVRAY, Ross T.A.
7 MASON, Anne B.
8 WOODWORTH, Robert C.
9
10 (ii) TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
11 MOLECULES AND MUTANTS THEREOF
12
13 (iii) NUMBER OF SEQUENCES: 7
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: LAHIVE & COCKFIELD
17 (B) STREET: 60 State Street, suite 510
18 (C) CITY: Boston
19 (D) STATE: Massachusetts
20 (E) COUNTRY: USA
21 (F) ZIP: 02109
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: ASCII text
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: 09/439,740
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 08/175,158
36 (B) FILING DATE:
37 (C) CLASSIFICATION:
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: DeConti, Giulio A.
41 (B) REGISTRATION NUMBER: 31,503
42 (C) REFERENCE/DOCKET NUMBER: UVI-005CP2
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (617) 227-7400
46 (B) TELEFAX: (617) 227-5941

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47
48
49 (2) INFORMATION FOR SEQ ID NO:1:
50
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 2327 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear
56
57 (ii) MOLECULE TYPE: cDNA
58
59
60 (ix) FEATURE:
61 (A) NAME/KEY: CDS
62 (B) LOCATION: 31..2124
63
64 (ix) FEATURE:
65 (A) NAME/KEY: mat_peptide
66 (B) LOCATION: 88..2124
67
68
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70
71 TGTGCTCGCT GCTCAGCGCG CACCCGGAAG ATG AGG CTC GCC GTG GGA GCC CTG 54
72 Met Arg Leu Ala Val Gly Ala Leu
73 -19 -15
74
75 CTG GTC TGC GCC GTC CTG GGG CTG TGT CTG GCT GTC CCT GAT AAA ACT 102
76 Leu Val Cys Ala Val Leu Gly Leu Cys Leu Ala Val Pro Asp Lys Thr
77 -10 -5 1 5
78
79 GTG AGA TGG TGT GCA GTG TCG GAG CAT GAG GCC ACT AAG TGC CAG AGT 150
80 Val Arg Trp Cys Ala Val Ser Glu His Glu Ala Thr Lys Cys Gln Ser
81 10 15 20
82
83 TTC CGC GAC CAT ATG AAA AGC GTC ATT CCA TCC GAT GGT CCC AGT GTT 198
84 Phe Arg Asp His Met Lys Ser Val Ile Pro Ser Asp Gly Pro Ser Val
85 25 30 35
86
87 GCT TGT GTG AAG AAA GCC TCC TAC CTT GAT TGC ATC AGG GCC ATT GCG 246
88 Ala Cys Val Lys Lys Ala Ser Tyr Leu Asp Cys Ile Arg Ala Ile Ala
89 40 45 50
90
91 GCA AAC GAA GCG GAT GCT GTG ACA CTG GAT GCA GGT TTG GTC TAT GAT 294
92 Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala Gly Leu Val Tyr Asp
93 55 60 65
94
95 GCT TAC TTG GCT CCC AAT AAC CTG AAG CCT GTG GTG GCA GAG TTC TAT 342
96 Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val Val Ala Glu Phe Tyr
97 70 75 80 85
98
99 GGG TCA AAA GAG GAT CCA CAG ACT TTC TAT TAT GCT GTT GCT GTG GTG 390

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100	Gly	Ser	Lys	Glu	Asp	Pro	Gln	Thr	Phe	Tyr	Tyr	Ala	Val	Ala	Val	Val	
101	90					95					100						
102																	
103	AAG	AAG	GAT	AGT	GGC	TTC	CAG	ATG	AAC	CAG	CTT	CGA	GGC	AAG	AAG	TCC	438
104	Lys	Lys	Asp	Ser	Gly	Phe	Gln	Met	Asn	Gln	Leu	Arg	Gly	Lys	Lys	Ser	
105	105						110					115					
106																	
107	TGC	CAC	ACG	GGT	CTA	GGC	AGG	TCC	GCT	GGG	TGG	AAC	ATC	CCC	ATA	GGC	486
108	Cys	His	Thr	Gly	Leu	Gly	Arg	Ser	Ala	Gly	Trp	Asn	Ile	Pro	Ile	Gly	
109	120					125					130						
110																	
111	TTA	CTT	TAC	TGT	GAC	TTA	CCT	GAG	CCA	CGT	AAA	CCT	CTT	GAG	AAA	GCA	534
112	Leu	Leu	Tyr	Cys	Asp	Leu	Pro	Glu	Pro	Arg	Lys	Pro	Leu	Glu	Lys	Ala	
113	135						140					145					
114																	
115	GTG	GCC	AAT	TTC	TTC	TCG	GGC	AGC	TGT	GCC	CCT	TGT	GCG	GAT	GGG	ACC	582
116	Val	Ala	Asn	Phe	Phe	Ser	Gly	Ser	Cys	Ala	Pro	Cys	Ala	Asp	Gly	Thr	
117	150					155					160					165	
118																	
119	GAC	TTC	CCC	CAG	CTG	TGT	CAA	CTG	TGT	CCA	GGG	TGT	GGC	TGC	TCC	ACC	630
120	Asp	Phe	Pro	Gln	Leu	Cys	Gln	Leu	Cys	Pro	Gly	Cys	Gly	Cys	Ser	Thr	
121	170					175					180						
122																	
123	CTT	AAC	CAA	TAC	TTC	GGC	TAC	TCG	GGA	GCC	TTC	AAG	TGT	CTG	AAG	GAT	678
124	Leu	Asn	Gln	Tyr	Phe	Gly	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Lys	Asp	
125	185						190					195					
126																	
127	GGT	GCT	GGG	GAT	GTG	GCC	TTT	GTC	AAG	CAC	TCG	ACT	ATA	TTT	GAG	AAC	726
128	Gly	Ala	Gly	Asp	Val	Ala	Phe	Val	Lys	His	Ser	Thr	Ile	Phe	Glu	Asn	
129	200					205					210						
130																	
131	TTG	GCA	AAC	AAG	GCT	GAC	AGG	GAC	CAG	TAT	GAG	CTG	CTT	TGC	CTA	GAC	774
132	Leu	Ala	Asn	Lys	Ala	Asp	Arg	Asp	Gln	Tyr	Glu	Leu	Leu	Cys	Leu	Asp	
133	215						220					225					
134																	
135	AAC	ACC	CGG	AAG	CCG	GTA	GAT	GAA	TAC	AAG	GAC	TGC	CAC	TTG	GCC	CAG	822
136	Asn	Thr	Arg	Lys	Pro	Val	Asp	Glu	Tyr	Lys	Asp	Cys	His	Leu	Ala	Gln	
137	230					235					240					245	
138																	
139	GTC	CCT	TCT	CAT	ACC	GTC	GTG	GCC	CGA	AGT	ATG	GGC	GGC	AAG	GAG	GAC	870
140	Val	Pro	Ser	His	Thr	Val	Val	Ala	Arg	Ser	Met	Gly	Gly	Lys	Glu	Asp	
141	250					255					260						
142																	
143	TTG	ATC	TGG	GAG	CTT	CTC	AAC	CAG	GCC	CAG	GAA	CAT	TTT	GGC	AAA	GAC	918
144	Leu	Ile	Trp	Glu	Leu	Leu	Asn	Gln	Ala	Gln	Glu	His	Phe	Gly	Lys	Asp	
145	265						270					275					
146																	
147	AAA	TCA	AAA	GAA	TTC	CAA	CTA	TTC	AGC	TCT	CCT	CAT	GGG	AAG	GAC	CTG	966
148	Lys	Ser	Lys	Glu	Phe	Gln	Leu	Phe	Ser	Ser	Pro	His	Gly	Lys	Asp	Leu	
149	280					285					290						
150																	
151	CTG	TTT	AAG	GAC	TCT	GCC	CAC	GGG	TTT	TTA	AAA	GTC	CCC	CCA	AGG	ATG	1014
152	Leu	Phe	Lys	Asp	Ser	Ala	His	Gly	Phe	Leu	Lys	Val	Pro	Pro	Arg	Met	

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	295	300	305	
153				
154				
155	GAT GCC AAG ATG TAC CTG GGC TAT GAG TAT GTC ACT GCC ATC CGG AAT			1062
156	Asp Ala Lys Met Tyr Leu Gly Tyr Glu Tyr Val Thr Ala Ile Arg Asn			
157	310	315	320	325
158				
159	CTA CGG GAA GGC ACA TGC CCA GAA GCC CCA ACA GAT GAA TGC AAG CCT			1110
160	Leu Arg Glu Gly Thr Cys Pro Glu Ala Pro Thr Asp Glu Cys Lys Pro			
161	330	335	340	
162				
163	GTG AAG TGG TGT GCG CTG AGC CAC CAC GAG AGG CTC AAG TGT GAT GAG			1158
164	Val Lys Trp Cys Ala Leu Ser His His Glu Arg Leu Lys Cys Asp Glu			
165	345	350	355	
166				
167	TGG AGT GTT AAC AGT GTA GGG AAA ATA GAG TGT GTA TCA GCA GAG ACC			1206
168	Trp Ser Val Asn Ser Val Gly Lys Ile Glu Cys Val Ser Ala Glu Thr			
169	360	365	370	
170				
171	ACC GAA GAC TGC ATC GCC AAG ATC ATG AAT GGA GAA GCT GAT GCC ATG			1254
172	Thr Glu Asp Cys Ile Ala Lys Ile Met Asn Gly Glu Ala Asp Ala Met			
173	375	380	385	
174				
175	AGC TTG GAT GGA GGG TTT GTC TAC ATA GCG GGC AAG TGT GGT CTG GTG			1302
176	Ser Leu Asp Gly Gly Phe Val Tyr Ile Ala Gly Lys Cys Gly Leu Val			
177	390	395	400	405
178				
179	CCT GTC TTG GCA GAA AAC TAC AAT AAG AGC GAT AAT TGT GAG GAT ACA			1350
180	Pro Val Leu Ala Glu Asn Tyr Asn Lys Ser Asp Asn Cys Glu Asp Thr			
181	410	415	420	
182				
183	CCA GAG GCA GGG TAT TTT GCT GTA GCA GTG GTG AAG AAA TCA GCT TCT			1398
184	Pro Glu Ala Gly Tyr Phe Ala Val Ala Val Val Lys Lys Ser Ala Ser			
185	425	430	435	
186				
187	GAC CTC ACC TGG GAC AAT CTG AAA GGC AAG AAG TCC TGC CAT ACG GCA			1446
188	Asp Leu Thr Trp Asp Asn Leu Lys Gly Lys Lys Ser Cys His Thr Ala			
189	440	445	450	
190				
191	GTT GGC AGA ACC GCT GGC TGG AAC ATC CCC ATG GGC CTG CTC TAC AAT			1494
192	Val Gly Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Tyr Asn			
193	455	460	465	
194				
195	AAG ATC AAC CAC TGC AGA TTT GAT GAA TTT TTC AGT GAA GGT TGT GCC			1542
196	Lys Ile Asn His Cys Arg Phe Asp Glu Phe Phe Ser Glu Gly Cys Ala			
197	470	475	480	485
198				
199	CCT GGG TCT AAG AAA GAC TCC AGT CTC TGT AAG CTG TGT ATG GGC TCA			1590
200	Pro Gly Ser Lys Lys Asp Ser Ser Leu Cys Lys Leu Cys Met Gly Ser			
201	490	495	500	
202				
203	GGC CTA AAC CTG TGT GAA CCC AAC AAC AAA GAG GGA TAC TAC GGC TAC			1638
204	Gly Leu Asn Leu Cys Glu Pro Asn Asn Lys Glu Gly Tyr Tyr Gly Tyr			
205	505	510	515	

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
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SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

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SEQUENCE CORRECTION REPORT
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Line

Original Text

Corrected Text